

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: /o Source: Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual - ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/.049,988	
ATTN: NEW RULES CASE	S: Please disregard english "Alpha" headers, which were inserted by pto softw	ARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces,	
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
SVariable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7Skipped Sequences (OLD RULES)	Sequence(s)missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	•
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.	
Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220><223> section is required when <213> response is Unknown or is Artificial Sequence	• •,
11Use of <220>	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy lile to floppy disk.	
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	
	AMC/MH - Biotechnology Systems Branch - 08/21/2001	



PCT/A

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,988

DATE: 03/05/2002

TIME: 14:00:57

pr1,3-6

Input Set : A:\seqlist-1.txt

Output Set: N:\CRF3\03052002\J049988.raw

Does Not Comply Corrected Diskette Needec

3 <110> APPLICANT: Biosyn Arzneimittel GmbH

5 <120> TITLE OF INVENTION: Nucleic acid molecule comprising a nucleic acid sequence

which codes for a haemocyanin, and comprising at least one

intron sequence

9 <130> FILE REFERENCE: PCT1220-01966

-> 11 <140> CURRENT APPLICATION NUMBER: US/10/049,988

> 12 <141> CURRENT FILING DATE: 2002-02-20

14 <160> NUMBER OF SEQ ID NOS: 108

16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

412 <210> SEQ ID NO: 15

413 <211> LENGTH: 1546

414 <212> TYPE: DNA

415 <213> ORGANISM: Haliotis tuberculata

417 <400> SEQUENCE: 15

418 ageccacaga ggaccagttg aagaaacaga agtcactege caacatactg aeggcaatge 60

419 acactttcat cgtaaggaag ttgattcgct gtccctggat gaagcaaaca acttgaagaa 120

420 tgccctttac aagctacaga acgaccacag tctaacggga tacgaagcaa tctctggtta 180

421 ccatggatac cccaatctgt gtccggaaga aggcgatgac aaaatacccc tgctgcgtcc 240

422 ccggatgggc atctttcctt actggcacag actcttgacc attcaactgg aaagagctct 300 423 tgagcacaat ggtgcactgc ttggtgttcc ttactgggac tggaacaagg acctgtcgtc 360

424 actgccggcg ttcttctccg actccagcaa caacaatccc tacttcaagt accacatcgc 420

425 cggtgttggt cacgacaccg tcagagagcc aactagtctt atatataacc agccccaaat 480

426 ccatggttat gattatetet attacetage attgaceaeg ettgaagaaa acaattactg 540

427 ggactttgag gttcagtatg agatcctcca caacgccgtc cactcctggc ttggaggatc 600

428 ccagaagtat tccatgtcta ccctggagta ttcggccttt gaccctgtct ttatgatcct 660

429 tcactcgggt ctagacagac tttggatcat ctggcaagaa cttcagaaga tcaggagaaa 720

430 gccctacaac ttcgctaaat gtgcttatca tatgatggaa gagccactgg cgcccttcag 780

431 ctatecatet ateaaceagg acgagtteae eegtgeeaae teeaageett etaeagtttt 840

432 tgacagccat aagttcggct accattacga taacctgaat gttagaggtc acagcatcca 900

433 agaactcaac acaatcatca atgacttgag aaacacagac agaatctacg caggatttgt 960

434 tttgtcaggc atcggtacgt ctgctagtgt caagatctat ctccgaacag atgacaatga 1020

435 cgaagaagtt ggaactttca ctgtcctggg aggagagag gaaatgccat gggcctacga 1080

436 gcgagttttc aagtatgaca tcacagaggt tgcagataga cttaaaatta agttatgggg 1140

437 acaccettta actteeggaa etggagatea cateettaeg aatggaateg gtggtaaaca 1200 438 agagectace caaateettt cateatetae agacetgeea ateatqaeta egatgttett 1260

E--> 439 gttatcccag tanggaagaa accttcacat ccctcccaaa gttgtcgtca agaaaggcac 1320

440 ccgcatcgag ttccacccag tcgatgattc agttacgaga ccagttgttg atcttggaag 1380

441 ctacactgca ctcttcaact gtgtggtacc accgttcaca taccacggat tcgaactgaa 1440

442 ccacqtctat tctqtcaagc ctqqtqacta ctatqttact qqacccacqa qaqacctttq 1500

Jen 9 on Ever Sunnay Sheet

Input Set : A:\seqlist-1.txt

Output Set: N:\CRF3\03052002\J049988.raw

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DATE: 03/05/2002

TIME: 14:00:57

Input Set : A:\seqlist-1.txt Output Set: N:\CRF3\03052002\J049988.raw 1926 1928 Glu Arg Glu Met Pro Trp Ala Tyr Glu Arg Val Phe Lys Tyr Asp Ile 1929 355 360 1931 Thr Glu Val Ala Asp Arg Leu Lys Ile Lys Leu Trp Gly His Pro Leu 370 375 1932 1934 Thr Ser Gly Thr Gly Asp His Ile Leu Thr Asn Gly Ile Gly Gly Lys 390 395 1935 385 1937 Gln Glu Pro Thr Gln Ile Leu Ser Ser Ser Thr Asp Leu Pro Ile Met 415 1938 405 410 E--> 1940 Thr Thr Met Phe Leu Leu Ser Gln (Xaa Gly Arg Asn Leu His Ile Pro 1941 420 1943 Pro Lys Val Val Val Lys Lys Gly Thr Arg Ile Glu Phe His Pro Val 435 440 1946 Asp Asp Ser Val Thr Arg Pro Val Val Asp Leu Gly Ser Tyr Thr Ala 460 450 455 1949 Leu Phe Asn Cys Val Val Pro Pro Phe Thr Tyr His Gly Phe Glu Leu 470 475 1952 Asn His Val Tyr Ser Val Lys Pro Gly Asp Tyr Tyr Val Thr Gly Pro 490 1955 Thr Arg Asp Leu Cys Gln Asn Ala Asp Val Arg Ile His Ile His Val 500 505 1958 Glu Asp Glu 1959 515 2852 <210> SEQ ID NO: 62 2853 <211> LENGTH: 1185 2854 <212> TYPE: DNA 2855 <213> ORGANISM: Haliotis tuberculata 2857 <400> SEQUENCE: 62 2858 atcatattgc tggcagtgga gtcaggaaag acgtgacgtc tcttaccgca tctgagatag 60 2859 agaacctgag gcatgctctg caaagcgtga tggatgatga tggacccaat ggattccagg 120 E--> 2860 caattgctgc ttatcacgga agtcctccca tgtgtcacat gcmtgatggt agagacgttg 180 2861 catgttgtac tcatggaatg gcatctttcc ctcactggca cagactgttt gtgaaacaga 240 2862 tggaggatgc actggctgcg catggagctc acattggcat accatactgg gattggacaa 300 2863 gtgcgtttag tcatctgcct gccctagtga ctgaccacga gcacaatccc ttccaccacg 360 2864 gacatattgc tcatcggaat gtggatacat ctcgatctcc gagagacatg ctgttcaatg 420 2865 accccgaaca cgggtcagaa tcattcttct atagacaggt tctcttggct ctagaacaga 480 2866 cagacttctg ccaatttgaa gttcagtttg aaataacaca caatgcaatc cactcttgga 540 2867 ctggaggaca tactccatat ggaatgtcat cactggaata tacagcatat gatccactct 600 2868 tttatctcca ccattccaac actgatcgta tctgggccat ctggcaggca ctccagaaat 660 2869 acagaggttt tcaatacaac gcagctcatt gcgatatcca ggttctgaaa caacctctta 720 2870 aaccattcag cgagtccagg aatccaaacc cagtcaccag agccaattct agggcagtcg 780 2871 attcatttga ttatgagaga ctcaattatc aatatgacac acttaccttc cacggacatt 840 2872 ctatctcaga acttgatgcc atgcttcaag agagaaagaa ggaagagaga acatttgcag 900 2873 ccttcctgtt gcacggattt ggcgccagtg ctgatgtttc gtttgatgtc tgcacacctg 960 2874 atggtcattg tgcctttgct ggaaccttcg cggtacttgg tggggagctt gagatgccct 1020 2875 ggtcctttga aagattgttc cgttacgata tcacaaaggt tctcaagcag atgaatcttc 1080 2876 actatgattc tgagttccac tttgagttga agattgttgg cacagatgga acagaactgc 1140 2877 catcggatcg tatcaagagc cctaccattg aacaccatgg aggag 1185 4137 <210> SEQ ID NO: 79

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,988

Input Set : A:\seqlist-l.txt

Output Set: N:\CRF3\03052002\J049988.raw

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4138 <211> LENGTH: 395
    4139 <212> TYPE: PRT
    4140 <213> ORGANISM: Megathura crenulata
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                     20
    4149 Asp Asp Gly Pro Asn Gly Phe Gln Ala Ile Ala Ala Tyr His Gly Ser
    4150 35
                                     40
                                                                              -Titem 9
E--> 4152 Pro Pro Met Cys His Met (Xaa Asp Gly Arg Asp Val Ala Cys Cys Thr
     4155 His Gly Met Ala Ser Phe Pro His Trp His Arg Leu Phe Val Lys Gln
    4158 Met Glu Asp Ala Leu Ala Ala His Gly Ala His Ile Gly Ile Pro Tyr
    4161 Trp Asp Trp Thr Ser Ala Phe Ser His Leu Pro Ala Leu Val Thr Asp
                                        105
                    100
    4164 His Glu His Asn Pro Phe His His Gly His Ile Ala His Arg Asn Val
                115
                                    120
    4167 Asp Thr Ser Arg Ser Pro Arg Asp Met Leu Phe Asn Asp Pro Glu His
          130
                                 135
                                                    140
    4170 Gly Ser Glu Ser Phe Phe Tyr Arg Gln Val Leu Leu Ala Leu Glu Gln
                             150
                                                155
    4173 Thr Asp Phe Cys Gln Phe Glu Val Gln Phe Glu Ile Thr His Asn Ala
                         165
                                             170
    4176 Ile His Ser Trp Thr Gly Gly His Thr Pro Tyr Gly Met Ser Ser Leu
                     180
                                         185
    4179 Glu Tyr Thr Ala Tyr Asp Pro Leu Phe Tyr Leu His His Ser Asn Thr
          195
                                     200
    4182 Asp Arg Ile Trp Ala Ile Trp Gln Ala Leu Gln Lys Tyr Arg Gly Phe
                                 215
    4185 Gln Tyr Asn Ala Ala His Cys Asp Ile Gln Val Leu Lys Gln Pro Leu
                             230
                                                 235
    4188 Lys Pro Phe Ser Glu Ser Arg Asn Pro Asn Pro Val Thr Arg Ala Asn
                         245
                                             250
     4191 Ser Arg Ala Val Asp Ser Phe Asp Tyr Glu Arg Leu Asn Tyr Gln Tyr
                    260
                                         265
    4194 Asp Thr Leu Thr Phe His Gly His Ser Ile Ser Glu Leu Asp Ala Met
                275
                                     280
    4197 Leu Gln Glu Arg Lys Lys Glu Glu Arg Thr Phe Ala Ala Phe Leu Leu
                                 295
    4200 His Gly Phe Gly Ala Ser Ala Asp Val Ser Phe Asp Val Cys Thr Pro
                             310
                                                 315
    4203 Asp Gly His Cys Ala Phe Ala Gly Thr Phe Ala Val Leu Gly Gly Glu
                                             330
    4206 Leu Glu Met Pro Trp Ser Phe Glu Arg Leu Phe Arg Tyr Asp Ile Thr
    4207 340
                                 345
    4209 Lys Val Leu Lys Gln Met Asn Leu His Tyr Asp Ser Glu Phe His Phe
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Input Set : A:\seqlist-1.txt

Output Set: N:\CRF3\03052002\J049988.raw

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4210
                 355
                                     360
    4212 Glu Leu Lys Ile Val Gly Thr Asp Gly Thr Glu Leu Pro Ser Asp Arg
             370
                                 375
     4215 Ile Lys Ser Pro Thr Ile Glu His His Gly Gly
     4216 385
                             390
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     4638 <211> LENGTH: 1548
     4639 <212> TYPE: DNA
     4640 <213> ORGANISM: Haliotis tuberculata
    4642 <400> SEQUENCE: 95
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     4644 gcacactttc atcgtaagga agttgattcg ctgtccctgg atgaagcaaa caacttgaag 120
     4645 aatgeeettt acaagetaca gaacgaeeac agtetaaegg gatacgaage aatetetggt 180
     4646 taccatggat accccaatct gtgtccggaa gaaggcgatg acaaaatacc cctgctgcgt 240
     4647 ccccggatgg gcatctttcc ttactggcac agactcttga ccattcaact ggaaagagct 300
     4648 cttgagcaca atggtgcact gcttggtgtt ccttactggg actggaacaa ggacctgtcg 360
     4649 tcactgecgg cgttcttctc cgactccagc aacaacaatc cctacttcaa gtaccacatc 420
     4650 gccggtgttg gtcacgacac cgtcagagag ccaactagtc ttatatataa ccagccccaa 480
     4651 atccatggtt atgattatct ctattaccta gcattgacca cgcttgaaga aaacaattac 540
     4652 tgggactttg aggttcagta tgagatcctc cacaacgccg tccactcctg gettggagga 600
     4653 toccagaagt attocatgte taccetggag tatteggeet ttgaccetgt etttatgate 660
     4654 cttcactcgg gtctagacag actttggatc atctggcaag aacttcagaa gatcaggaga 720
     4655 aagccctaca acttcgctaa atgtgcttat catatgatgg aagagccact ggcgcccttc 780
     4656 agctatocat ctatoaacca ggacgagtto accogtgooa actocaagco ttotacagtt 840
     4657 tttgacagcc ataagttcgg ctaccattac gataacctga atgttagagg tcacagcatc 900
     4658 caaqaactca acacaatcat caatqacttq aqaaacacaq acaqaatcta cqcaqqattt 960
     4659 gttttgtcag gcatcggtac gtctgctagt gtcaagatct atctccgaac agatgacaat 1020
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     4661 gagcgagttt tcaagtatga catcacagag gttgcagata gacttaaaat taagttatgg 1140
     4662 ggacaccett taactteegg aactggagat cacateetta egaatggaat eggtggtaaa 1200
     4663 caagageeta eeca<u>aateet tteateatet acagacetge caateatgae taegatgtte 1260</u>
E--> 4664 ttgttatccc agtanggaag aaaccttcac atccctccca aagttgtcgt caagaaaggc 1320
     4665 accegeateg agttecacce agtegatgat teagttaega gaceagttgt tgatettgga 1380
     4666 agetacactg cactetteaa etgtgtggta eeacegttea eataceaegg attegaaetg 1440
     4667 aaccacgtct attctgtcaa gcctggtgac tactatgtta ctggacccac gagagacctt 1500
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     4963 <212> TYPE: DNA
     4964 <213> ORGANISM: Megathura crenulata
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     4970 gcatgttgta ctcatggaat ggcatctttc cctcactggc acagactgtt tgtgaaacag 240
     4971 atggaggatg cactggctgc gcatggagct cacattggca taccatactg ggattggaca 300
     4972 agtgcgttta gtcatctgcc tgccctagtg actgaccacg agcacaatcc cttccaccac 360
     4973 ggacatattg ctcatcggaa tgtggataca tctcgatctc cgagagacat gctgttcaat 420
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Input Set : A:\seqlist-l.txt

.

Output Set: N:\CRF3\03052002\J049988.raw

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     4977 ttttatctcc accattccaa cactgatcgt atctgggcca tctggcaggc actccagaaa 660
     4978 tacagaggtt ttcaatacaa cgcagctcat tgcgatatcc aggttctgaa acaacctctt 720
     4979 aaaccattca gcgagtccag gaatccaaac ccagtcacca gagccaattc tagggcagtc 780
     4980 gattcatttg attatgagag actcaattat caatatgaca cacttacctt ccacggacat 840
     4981 tctatctcag aacttgatgc catgcttcaa gagagaaaga aggaagagag aacatttgca 900
     4982 gccttcctgt tgcacqgatt tggcgccagt gctgatgttt cgtttgatgt ctgcacacct 960
     4983 gatggtcatt gtgcctttgc tggaaccttc gcggtacttg gtggggagct tgagatgccc 1020
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     4985 cactatgatt ctgagttcca ctttgagttg aagattgttg gcacagatgg aacagaactg 1140
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     4990 <212> TYPE: DNA
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     4996 aatggatatg aatcaatagc cggttaccat ggctatccat teetetgeec tgaacatggt 180
     4997 gaagaccagt acgcatgctg tgtccacgga atgcctgtat ttccacattg gcacagactt 240
     4998 catacaatce agtttgagag agctctcaaa gaacatggtt ctcatttggg tctgccatac 300
     4999 tgggactgg
E--> 5005(8)
```

KY1

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

4

VERIFICATION SUMMARY

DATE: 03/05/2002

PATENT APPLICATION: US/10/049,988

TIME: 14:00:59

Input Set : A:\seqlist-l.txt

Output Set: N:\CRF3\03052002\J049988.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:439 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15 L:1940 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39 L:2860 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62 L:4152 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:79 L:4664 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:95 L:4969 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:107 L:5005 M:254 E: No. of Bases conflict, LENGTH:Input:8 Counted:309 SEQ:108